

SEQUENCE PROTOCOL

110 > Degussa AG

5 1120 > New nucleotide sequences which code for the menE gene

130 > 000551 BT

140 >

10 141 >

160 > 4

170 > PatentIn Ver. 2.1

15 210 > 1

211 > 1570

212 > DNA

213 > Corynebacterium glutamicum

20 210 >

211 > CDS

212 > (230)..(1357)

213 > menE gene

25 400 > 1

ttcgttgcga tagacatgct cttcgcagca ctgtttgcgc acgttccttc cggcatcttt 60

30 401 > 1570

gttaccaaca atggttggga actcaccggc gcaatcgccg ctggcgccgt gcttctcata 120

gcaatcgccg caggtgcattg gacatcgac ggggtctgg caaaacgcaa ggcataaatac 180

tagcgccaca actccgaatt ctgaaccatc ggcactagaa tctcgaaat atg sat act 248

Met Asn Thr

35 1

cgc gtc ctc gaa gca cta cct gtt gat ctt gca gat ccc acc gca att 286
Arg Val Leu Glu Ala Leu Pro Val Asp Leu Asp Pro Thr Ala Ile

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ctg gga gat ctc gag gac gca atc tct ggg aag aaa act ttc ctc ccc 334
Leu Gly Asp Leu Glu Asp Ala Ile Ser Gly Lys Lys Thr Phe Leu Pro

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atc cct gta caa gat aaa acc cgt gca cag ttg ctg cgc gat tct caa 382
Ile Pro Val Gln Asp Lys Thr Arg Ala Gln Leu Leu Arg Asp Ser Gln

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cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc act 430
Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala Thr

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tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg aat 478
Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu Asn

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ttg	gtg	agt	tcc	gcc	gat	gtc	acg	cat	cag	ttt	tta	ggg	gaa	ggc	526		
Leu	Val	Ser	Ser	Ala	Asp	Ala	Thr	His	Gln	Phe	Ile	Gly	Gly	Glu			
85							90				95						
5	cag	tgg	tta	gcc	atg	cca	gca	cac	cac	att	gca	ggc	atg	cag	gtg	574	
	Gln	Trp	Leu	Leu	Ala	Met	Pro	Ala	His	His	Ile	Ala	Gly	Met	Ser		
	100					105					110				115		
10	ctt	ctt	cga	agc	ctc	att	gtc	gga	gtt	gag	cca	cta	gtc	atc	gtt	622	
	Leu	Leu	Arg	Ser	Leu	Ile	Ala	Gly	Val	Glu	Pro	Leu	Ala	Ile	Asp	Leu	
						120				125				130			
15	agc	aca	ggg	ttt	cac	att	gac	gtc	ttc	gca	ggc	gcc	ggg	gca	gaa	ctg	677
	Ser	Thr	Gly	Phe	His	Ile	Asp	Ala	Phe	Ala	Gly	Ala	Ala	Glu	Leu		
					135				140				145				
20	aaa	aat	acc	ggc	gac	cgc	gtc	tat	aca	tcc	ttg	act	cca	atg	cag	tta	714
	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser	Leu	Thr	Pro	Met	Gln	Leu	
					150				155				160				
25	ctt	aaa	gca	atg	gac	tcc	ttg	caa	ggc	att	gaa	gcc	ctg	aaa	ctt	ttt	766
	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile	Glu	Ala	Leu	Lys	Leu	Phe	
					165				170				175				
30	ttt	gtc	gag	cag	cta	gac	atc	aac	att	gtc	acc	acc	taa	ggc	tcc	tca	862
	Ser	Ala	Gly	Gln	Leu	Asp	Ile	Asn	Ile	Val	Thr	Thr	Tyr	Gly	Ser	Ser	
					200				205				210				
35	gag	act	tcc	ggg	tgc	gtt	tat	gat	ggc	aag	ccc	att	ccc	ggc	ggc	910	
	Gly	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly	Lys	Pro	Ile	Pro	Gly	Ala	
					215				220				225				
40	aaa	gtc	tgt	att	tcc	gat	gag	cgc	att	gag	ttg	ggc	ccg	atg	att	954	
	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu	Leu	Gly	Gly	Pro	Met	Ile	
					230				235				240				
45	ggc	cag	ggc	tac	aga	aat	gca	cct	gaa	cat	ccg	gat	tcc	gcc	aac	gag	1006
	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His	Pro	Asp	Phe	Ala	Asn	Glu	
					245				250				255				
50	ggc	tgg	ttt	acc	acc	tct	gat	tca	ggt	gaa	ctc	cac	gac	ggg	att	ctc	1054
	Gly	Trp	Phe	Thr	Ser	Asp	Ser	Gly	Glu	Leu	His	Asp	Gly	Ile	Leu		
					260				265				270			275	
55	acc	gtg	act	ggg	cgc	gtg	gat	acc	gtc	att	gat	tcc	ggg	ttg	aag	1102	
	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Val	Ile	Asp	Ser	Gly	Gly	Leu	Lys	
					280				285				290				
	ttg	cac	ccs	gag	gta	ctg	gaa	cgt	gcc	atc	gca	gat	att	aaa	ggg	gtc	1150
	Leu	His	Prc	Glu	Val	Leu	Glu	Arg	Ala	Ile	Ala	Asp	Ile	Lys	Gly	Val	
					295				300				305				
	acc	gcg	gcg	tgt	gtg	ggt	att	ccc	gat	ccc	ccg	tta	ggc	caa	gca	1198	
	Thr	Ala	Ala	Cys	Val	Val	Gly	Ile	Pro	Asp	Pro	Arg	Leu	Gly	Gln	Ala	
					310				315				320				

att gtg gcc gcg tac tcc gga tcc atc agt ccg tct gaa gtt att gaa 1246
 Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu
 325 330 335

5
 9gc ctc gac gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat 1294
 Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His
 340 345 350 355

10 att gaa tct ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct 1342
 Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala
 360 365 370

15 atc gag aag ctg ttt tagtcttcat tttgtgtggc tgcaactagt tttgcacat 1397
 Ile Ala Lys Leu Phe
 375

20 atccatcggt gtacactttg gogatctgtc catcattcc acccatgagg gtgtgtccaa 1457
 caactagtgc tccacttgg gtgggtggca cgacacgcaa gtgtcgccgc tgagcgtaga 1517
 cttggcgaat agggtgatca gagcgcagtg cgccaggcatg cagccatacg tca 1570

25 <210> 2
 <211> 376
 <212> PRT
 <213> Corynebacterium glutamicum

30 <400> 2
 Met Asn Thr Arg Val Leu Glu Ala Leu Pro Val Asp Leu Ala Asp Pro
 1 5 10 15

35 Thr Ala Ile Leu Gly Asp Leu Glu Asp Ala Ile Ser Gly Lys Lys Thr
 20 25 30

Phe Leu Pro Ile Pro Val Gln Asp Lys Thr Arg Ala Gln Leu Leu Arg
 35 40 45

40 Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val
 50 55 60

Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr
 65 70 75 80

45 Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly
 85 90 95

50 Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly
 100 105 110

Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala
 115 120 125

55 Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala
 130 135 140

Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro
 145 150 155 160

Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu
 165 170 175
 5 Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln
 180 185 190
 Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr
 195 200 205
 10 Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile
 210 215 220
 15 Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly
 225 230 235 240
 Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe
 245 250 255
 20 Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp
 260 265 270
 Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Val Ile Asp Ser Gly
 275 280 285
 25 Gly Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile
 290 295 300
 30 Lys Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu
 305 310 315 320
 Gly Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu
 325 330 335
 35 Val Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg
 340 345 350
 Leu Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp
 355 360 365
 40 Arg Arg Ala Ile Ala Lys Leu Phe
 370 375
 45 .J10. 3
 .J11. 19
 .J12. DNA
 .J13. Corynebacterium glutamicum
 50 .J20.
 .J21. Primer menE-int1
 55 .J03. 3
 .J04. tcaatcgt tgaatttgg 19
 .J10. 4
 .J11. 19

·1212· DNA

·1213· *Corynebacterium glutamicum*

·1220·

5 ·1223· Primer menE-int2

·1400· 4

caggtgcatt tctgtagcc

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